

ABSTRACT OF THE INVENTION

The invention relates to computer-based systems and methods for the design, comparison and analysis of genetic and proteomic databases. In a particular embodiment, the recited systems and methods have been implemented in a computer tool called ARROGANT. ARROGANT, in the analysis mode, is a comprehensive tool for providing annotation to large gene and protein collections. ARROGANT takes in a large collection of sequence identifiers and associates it with other information collected from many sources like sequence annotations, pathways, homology, polymorphisms, artifacts, etc. The simultaneous annotation for a large assembly of genes makes the collection of genomic / EST sequences truly informative.